



SEQUENCE LISTING

RECEIVED
AUG 27 2001
TECH CENTER 1600/2900

<110> Walsh, Christopher
Chao, Hengjun
Burstein, Haim
Lynch, Carmel
Stepan, Tony
Munson, Keith

<120> Adeno-Associated Virus Vectors Encoding Factor VIII and
Methods of Using Same

<130> 35052/204375

<140> US 09/689,430

<141> 2000-10-12

<150> 60/158,780

<151> 1999-10-12

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 7944

<212> DNA

<213> Artificial Sequence

<220>

<223> Plasmid pDLZ6 encoding Homo sapiens BDD FVIII

<221> CDS

<222> (420)...(4835)

<400> 1

```
tggccactcc ctctctgcgc gctcgtcgc tcaactgaggc cgggcgacca aaggctgccc 60
gacgcccggg ctttgcccgg gcggcctcag tgagcgagcg agcgcgcaga gagggagtgg 120
ccaaactccat cactaggggt tcctcagatc tctttctaag taaacagtac atgaaccttt 180
accccgttgc tcggcaacgg cctgggtctgt gccaaagtgt tgctgacgca acccccactg 240
gctgggggctt ggccataggc catcagcgca tgcggatctc agtgtgggtt tgcaagagga 300
agcaaaaaagc ctctccaccc aggcctggaa tgtttccacc caatgtcgag cagtgtgggt 360
ttgcaagagg aagcaaaaag cctctccacc caggcctgga ctcgagagct tcgaccacc 419
atg caa ata gag ctc tcc acc tgc ttc ttt ctg tgc ctt ttg cga ttc 467
Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1 5 10 15

tgc ttt agt gcc acc aga aga tac tac ctg ggt gca gtg gaa ctg tca 515
Cys Phe Ser Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser
20 25 30

tgg gac tat atg caa agt gat ctc ggt gag ctg cct gtg gac gca aga 563
Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
35 40 45
```

ttt cct cct aga gtg cca aaa tct ttt cca ttc aac acc tca gtc gtg Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val 50 55 60	611
tac aaa aag act ctg ttt gta gaa ttc acg gtt cac ctt ttc aac atc Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Val His Leu Phe Asn Ile 65 70 75 80	659
gct aag cca agg cca ccc tgg atg ggt ctg cta ggt cct acc atc cag Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln 85 90 95	707
gct gag gtt tat gat aca gtg gtc att aca ctt aag aac atg gct tcc Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser 100 105 110	755
cat cct gtc agt ctt cat gct gtt ggt gta tcc tac tgg aaa gct tct His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser 115 120 125	803
gag gga gct gaa tat gat gat cag acc agt caa agg gag aaa gaa gat Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp 130 135 140	851
gat aaa gtc ttc cct ggt gga agc cat aca tat gtc tgg cag gtc ctg Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu 145 150 155 160	899
aaa gag aat ggt cca atg gcc tct gac cca ctg tgc ctt acc tac tca Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser 165 170 175	947
tat ctt tct cat gtg gac ctg gta aaa gac ttg aat tca ggc ctc att Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile 180 185 190	995
gga gcc cta cta gta tgt aga gaa ggg agt ctg gcc aag gaa aag aca Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr 195 200 205	1043
cag acc ttg cac aaa ttt ata cta ctt ttt gct gta ttt gat gaa ggg Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly 210 215 220	1091
aaa agt tgg cac tca gaa aca aag aac tcc ttg atg cag gat agg gat Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp 225 230 235 240	1139
gct gca tct gct cgg gcc tgg cct aaa atg cac aca gtc aat ggt tat Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr 245 250 255	1187
gta aac agg tct ctg cca ggt ctg att gga tgc cac agg aaa tca gtc Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val 260 265 270	1235

tat tgg cat gtg att gga atg ggc acc act cct gaa gtg cac tca ata	1283
Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile	
275 280 285	
ttc ctc gaa ggt cac aca ttt ctt gtg agg aac cat cgc cag gcg tcc	1331
Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser	
290 295 300	
ttg gaa atc tcg cca ata act ttc ctt act gct caa aca ctc ttg atg	1379
Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met	
305 310 315 320	
gac ctt gga cag ttt cta ctg ttt tgt cat atc tct tcc cac caa cat	1427
Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His	
325 330 335	
gat ggc atg gaa gct tat gtc aaa gta gac agc tgt cca gag gaa ccc	1475
Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro	
340 345 350	
caa cta cga atg aaa aat aat gaa gaa gcg gaa gac tat gat gat gat	1523
Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp	
355 360 365	
ctt act gat tct gaa atg gat gtg gtc agg ttt gat gat gac aac tct	1571
Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser	
370 375 380	
cct tcc ttt atc caa att cgc tca gtt gcc aag aag cat cct aaa act	1619
Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr	
385 390 395 400	
tgg gta cat tac att gct gct gaa gag gag gac tgg gac tat gct ccc	1667
Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro	
405 410 415	
tta gtc ctc gcc ccc gat gac aga agt tat aaa agt caa tat ttg aac	1715
Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn	
420 425 430	
aat ggc cct cag cgg att ggt agg aag tac aaa aaa gtc cga ttt atg	1763
Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met	
435 440 445	
gca tac aca gat gaa acc ttt aag act cgt gaa gct att cag cat gaa	1811
Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu	
450 455 460	
tca gga atc ttg gga cct tta ctt tat ggg gaa gtt gga gac aca ctg	1859
Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu	
465 470 475 480	
ttg att ata ttt aag aat caa gca agc aga cca tat aac atc tac cct	1907
Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro	
485 490 495	

cac gga atc act gat gtc cgt cct ttg tat tca agg aga tta cca aaa	1955
His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys	
500 505 510	
ggt gta aaa cat ttg aag gat ttt cca att ctg cca gga gaa ata ttc	2003
Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe	
515 520 525	
aaa tat aaa tgg aca gtg act gta gaa gat ggg cca act aaa tca gat	2051
Lys Tyr Lys Trp Thr Val Thr Glu Asp Gly Pro Thr Lys Ser Asp	
530 535 540	
cct cgg tgc ctg acc cgc tat tac tct agt ttc gtt aat atg gag aga	2099
Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg	
545 550 555 560	
gat cta gct tca gga ctc att ggc cct ctc ctc atc tgc tac aaa gaa	2147
Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu	
565 570 575	
tct gta gat caa aga gga aac cag ata atg tca gac aag agg aat gtc	2195
Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val	
580 585 590	
atc ctg ttt tct gta ttt gat gag aac cga agc tgg tac ctc aca gag	2243
Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu	
595 600 605	
aat ata caa cgc ttt ctc ccc aat cca gct gga gtg cag ctt gag gat	2291
Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp	
610 615 620	
cca gag ttc caa gcc tcc aac atc atg cac agc atc aat ggc tat gtt	2339
Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val	
625 630 635 640	
ttt gat agt ttg cag ttg tca gtt tgt ttg cat gag gtg gca tac tgg	2387
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp	
645 650 655	
tac att cta agc att gga gca cag act gac ttc ctt tct gtc ttc ttc	2435
Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe	
660 665 670	
tct gga tat acc ttc aaa cac aaa atg gtc tat gaa gac aca ctc acc	2483
Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr	
675 680 685	
cta ttc cca ttc tca gga gaa act gtc ttc atg tcg atg gaa aac cca	2531
Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro	
690 695 700	
ggt cta tgg att ctg ggg tgc cac aac tca gac ttt cgg aac aga ggc	2579
Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly	
705 710 715 720	

atg acc gcc tta ctg aag gtt tct agt tgt gac aag aac act ggt gat	2627
Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp	
725 730 735	
tat tac gag gac agt tat gaa gat att tca gca tac ttg ctg agt aaa	2675
Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys	
740 745 750	
aac aat gcc att gaa cca aga agc ttc tcc cag aat tca aga cac cct	2723
Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Pro	
755 760 765	
agc act agg caa aag caa ttt aat gcc acc cca cca gtc ttg aaa cgc	2771
Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Pro Pro Val Leu Lys Arg	
770 775 780	
cat caa cgg gaa ata act cgt act act ctt cag tca gat caa gag gaa	2819
His Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu	
785 790 795 800	
att gac tat gat gat acc ata tca gtt gaa atg aag aag gaa gat ttt	2867
Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe	
805 810 815	
gac att tat gat gag gat gaa aat cag agc ccc cgc agc ttt caa aag	2915
Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys	
820 825 830	
aaa aca cga cac tat ttt att gct gca gtg gag agg ctc tgg gat tat	2963
Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr	
835 840 845	
ggg atg agt agc tcc cca cat gtt cta aga aac agg gct cag agt ggc	3011
Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly	
850 855 860	
agt gtc cct cag ttc aag aaa gtt gtt ttc cag gaa ttt act gat ggc	3059
Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly	
865 870 875 880	
tcc ttt act cag ccc tta tac cgt gga gaa cta aat gaa cat ttg gga	3107
Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly	
885 890 895	
ctc ctg ggg cca tat ata aga gca gaa gtt gaa gat aat atc atg gta	3155
Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val	
900 905 910	
act ttc aga aat cag gcc tct cgt ccc tat tcc ttc tat tct agc ctt	3203
Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu	
915 920 925	
att tct tat gag gaa gat cag agg caa gga gca gaa cct aga aaa aac	3251
Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn	
930 935 940	

ttt gtc aag cct aat gaa acc aaa act tac ttt tgg aaa gtg caa cat	3299
Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His	
945 950 955 960	
cat atg gca ccc act aaa gat gag ttt gac tgc aaa gcc tgg gct tat	3347
His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr	
965 970 975	
ttc tct gat gtt gac ctg gaa aaa gat gtg cac tca ggc ctg att gga	3395
Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly	
980 985 990	
ccc ctt ctg gtc tgc cac act aac aca ctg aac cct gct cat ggg aga	3443
Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg	
995 1000 1005	
caa gtg aca gta cag gaa ttt gct ctg ttt ttc acc atc ttt gat gag	3491
Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu	
1010 1015 1020	
acc aaa agc tgg tac ttc act gaa aat atg gaa aga aac tgc agg gct	3539
Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala	
1025 1030 1035 1040	
ccc tgc aat atc cag atg gaa gat ccc act ttt aaa gag aat tat cgc	3587
Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg	
1045 1050 1055	
ttc cat gca atc aat ggc tac ata atg gat aca cta cct ggc tta gta	3635
Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val	
1060 1065 1070	
atg gct cag gat caa agg att cga tgg tat ctg ctc agc atg ggc agc	3683
Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser	
1075 1080 1085	
aat gaa aac atc cat tct att cat ttc agt gga cat gtg ttc act gta	3731
Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val	
1090 1095 1100	
cga aaa aaa gag gag tat aaa atg gca ctg tac aat ctc tat cca ggt	3779
Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly	
1105 1110 1115 1120	
gtt ttt gag aca gtg gaa atg tta cca tcc aaa gct gga att tgg cgg	3827
Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg	
1125 1130 1135	
gtg gaa tgc ctt att ggc gag cat cta cat gct ggg atg agc aca ctt	3875
Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr Leu	
1140 1145 1150	
ttt ctg gtg tac agc aat aag tgt cag act ccc ctg gga atg gct tct	3923
Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser	
1155 1160 1165	

gga cac att aga gat ttt cag att aca gct tca gga caa tat gga cag Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln 1170 1175 1180	3971
tgg gcc cca aag ctg gcc aga ctt cat tat tcc gga tca atc aat gcc Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala 1185 1190 1195 1200	4019
tgg agc acc aag gag ccc ttt tct tgg atc aag gtg gat ctg ttg gca Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala 1205 1210 1215	4067
cca atg att att cac ggc atc aag acc cag ggt gcc cgt cag aag ttc Pro Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe 1220 1225 1230	4115
tcc agc ctc tac atc tct cag ttt atc atc atg tat agt ctt gat ggg Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly 1235 1240 1245	4163
aag aag tgg cag act tat cga gga aat tcc act gga acc tta atg gtc Lys Lys Trp Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val 1250 1255 1260	4211
ttc ttt ggc aat gtg gat tca tct ggg ata aaa cac aat att ttt aac Phe Phe Gly Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn 1265 1270 1275 1280	4259
cct cca att att gct cga tac atc cgt ttg cac cca act cat tat agc Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser 1285 1290 1295	4307
att cgc agc act ctt cgc atg gag ttg atg ggc tgt gat tta aat agt Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser 1300 1305 1310	4355
tgc agc atg cca ttg gga atg gag agt aaa gca ata tca gat gca cag Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln 1315 1320 1325	4403
att act gct tca tcc tac ttt acc aat atg ttt gcc acc tgg tct cct Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro 1330 1335 1340	4451
tca aaa gct cga ctt cac ctc caa ggg agg agt aat gcc tgg aga cct Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro 1345 1350 1355 1360	4499
cag gtg aat aat cca aaa gag tgg ctg caa gtg gac ttc cag aag aca Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr 1365 1370 1375	4547
atg aaa gtc aca gga gta act act cag gga gta aaa tct ctg ctt acc Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr 1380 1385 1390	4595

agc atg tat gtg aag gag ttc ctc atc tcc agc agt caa gat ggc cat	4643
Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His	
1395 1400 1405	
cag tgg act ctc ttt ttt cag aat ggc aaa gta aag gtt ttt cag gga	4691
Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly	
1410 1415 1420	
aat caa gac tcc ttc aca cct gtg gtg aac tct cta gac cca ccg tta	4739
Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu	
1425 1430 1435 1440	
ctg act cgc tac ctt cga att cac ccc cag agt tgg gtg cac cag att	4787
Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile	
1445 1450 1455	
gcc ctg agg atg gag gtt ctg ggc tgc gag gca cag gac ctc tac tga	4835
Ala Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr *	
1460 1465 1470	
ctcgagcgcag ttctttctgag gggatcggca ataaaaagac agaataaaac gcacgggtgt	4895
tgggtcgttt gttcggatcc agatctagga acccctagtg atggagttgg ccaactccctc	4955
tctgcgcgct cgctcgctca ctgaggccgc ccgggcaaaag ccgggcgctc gggcgacctt	5015
tggtcgcccc gcctcagtga gcgagcgcgc gcgcagagag ggagtggcca accccccccc	5075
ccccccccct gcagcccagc tgcattaatg aatcggccaa cgcgcgggga gaggcggttt	5135
gcgtattggg cgctcttccg cttcctcgct cactgactcg ctgcgctcgg tcgttcggct	5195
gcggcgagcg gtatcagctc actcaaaggc ggtaatacgg ttatccacag aatcagggga	5255
taacgcagga aagaacatgt gagcaaaagg ccagcaaaag gccaggaacc gtaaaaaggc	5315
cgcgttgctg gcgtttttcc ataggctccg cccccctgac gagcatcaca aaaatcgacg	5375
ctcaagtcag aggtggcgaa acccgacagg actataaaga taccaggcgt ttccccctgg	5435
aagctccctc gtgcgctctc ctgttccgac cctgcccgtt accggatacc tgtccgcctt	5495
tctcccttcg ggaagcgtgg cgctttctca atgctcacgc tgtaggtatc tcagttcggg	5555
gtaggtcgtt cgctccaagc tgggctgtgt gcacgaacc ccggttcagc ccgaccgctg	5615
cgccttatcc ggtaactatc gtcttgagtc caaccggta agacacgact tatcgccact	5675
ggcagcagcc actggtaaca ggattagcag agcgagggtat gtaggcgggtg ctacagagtt	5735
cttgaagtgg tggcctaact acggctacac tagaaggaca gtatttggtg tctgcgctct	5795
gctgaagcca gttaccttcg gaaaaagagt tggtagctct tgatccggca aacaaaccac	5855
cgcgtgtagc ggtggttttt ttgtttgcaa gcagcagatt acgcgcagaa aaaaaggatc	5915
tcaagaagat cctttgatct tttctacggg gtctgacgct cagtggaaacg aaaactcacg	5975
ttaagggtatt ttggatcatg gattatcaaa aaggatcttc acctagatcc ttttaaatta	6035
aaaatgaagt tttaaatcaa tctaaagtat atatgagtaa acttggtctg acagttacca	6095
atgcttaatc agtgaggcac ctatctcagc gatctgtcta tttcgttcat ccatagttgc	6155
ctgactcccc gtgcgtgtaga taactacgat acgggagggc ttacatctg gccccagtg	6215
tgcaatgata ccgcgagacc cacgctcacc ggctccagat ttatcagcaa taaaccagcc	6275
agccggaagg gccgagcgca gaagtgggtc tgcaacttta tccgcctcca tccagtctat	6335
taattgttg cgggaagcta gagtaagtag ttccgcagtt aatagtttg gcaacgttgt	6395
tgccattgct acaggcatcg tgggtgtcag ctcgctggtt ggtatggctt cattcagctc	6455
cgtttcccaa cgatcaaggc gagttacatg atcccccatg ttgtgcaaaa aagcggttag	6515
ctccttcggt cctccgatcg ttgtcagaag taagttggcc gcagtgttat cactcatggt	6575
tatggcagca ctgcataatt ctcttactgt catgccatcc gtaagatgct tttctgtgac	6635
tgggtgagtac tcaaccaagt cattctgaga atagtgtatg cggcgaccga gttgctcttg	6695
cccggcgtca atacgggata ataccgcgc acatagcaga actttaaaaa tgctcatcat	6755
tggaaaaacgt tcttcggggc gaaaactctc aaggatctta ccgctgttga gatccagttc	6815
gatgtaaccc actcgtgcac ccaactgac ttccagcatct tttactttca ccagcgtttc	6875
tgggtgagca aaaacaggaa ggcaaaatgc cgcaaaaaag ggaataaggg cgacacggaa	6935
atgttgaata ctcatactct tcctttttca atattattga agcatttatc aggggttattg	6995


```

tctcatgagc ggatacatat ttgaatgtat ttagaaaaat aaacaaatag gggttccgcg 7055
cacatttccc cgaaaagtgc cacctgacgt ctaagaaacc attattatca tgacattaac 7115
ctataaaaaat aggcgtatca cgaggccctt tcgtctcgcg cgtttcggtg atgacggtga 7175
aaacctctga cacatgcagc tcccggagac gggtcacagct tgtctgtaag cggatgccgg 7235
gagcagacaa gcccgtcagg gcgcgtcagc ggggtgttggc ggggtgtcggg gctggcttaa 7295
ctatgcggca tcagagcaga ttgtactgag agtgcaccat atgcggtgtg aaataccgca 7355
cagatgcgta aggagaaaaat accgcatcag gaaattgtaa acgttaatat tttgttaaaa 7415
ttcgcgttaa atttttgtta aatcagctca ttttttaacc aataggccga aatcggcaaa 7475
atcccttata aatcaaaaaga atagaccgag atagggttga gtgttgttcc agtttggaac 7535
aagagtccac tattaaagaa cgtggactcc aacgtcaaag ggcgaaaaac cgtctatcag 7595
ggcgatggcc cactacgtga accatcaccc taatcaagtt ttttggggtc gaggtgccgt 7655
aaagcactaa atcggaaccc taaagggagc ccccgattta gagcttgacg gggaaagccg 7715
gcgaacgtgg cgagaaaagg agggaaagaa gcgaaaggag cgggcgctag gccgctggca 7775
agtgtagcgg tcacgctgcg cgtaaccacc acacccgccg cgcttaatgc gccgctacag 7835
ggcgcgtcgc gccattcgcc attcaggcta cgcaactgtt gggaagggcg atcgggtgcgg 7895
gcctcttcgc tattacgcca gctggctgca gggggggggg ggggggggt 7944

```

<210> 2

<211> 1471

<212> PRT

<213> Homo sapiens B-domain deleted factor VIII

<220>

<223> Homo sapiens BDD FVIII

<400> 2

```

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
 1           5           10          15
Cys Phe Ser Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser
 20          25          30
Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
 35          40          45
Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
 50          55          60
Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Val His Leu Phe Asn Ile
 65          70          75          80
Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
 85          90          95
Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
100         105         110
His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
115         120         125
Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
130         135         140
Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145         150         155         160
Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
165         170         175
Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
180         185         190
Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
195         200         205
Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
210         215         220
Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225         230         235         240

```

Ala	Ala	Ser	Ala	Arg	Ala	Trp	Pro	Lys	Met	His	Thr	Val	Asn	Gly	Tyr	
				245					250					255		
Val	Asn	Arg	Ser	Leu	Pro	Gly	Leu	Ile	Gly	Cys	His	Arg	Lys	Ser	Val	
			260					265					270			
Tyr	Trp	His	Val	Ile	Gly	Met	Gly	Thr	Thr	Pro	Glu	Val	His	Ser	Ile	
		275					280					285				
Phe	Leu	Glu	Gly	His	Thr	Phe	Leu	Val	Arg	Asn	His	Arg	Gln	Ala	Ser	
	290					295					300					
Leu	Glu	Ile	Ser	Pro	Ile	Thr	Phe	Leu	Thr	Ala	Gln	Thr	Leu	Leu	Met	
305					310					315					320	
Asp	Leu	Gly	Gln	Phe	Leu	Leu	Phe	Cys	His	Ile	Ser	Ser	His	Gln	His	
				325					330					335		
Asp	Gly	Met	Glu	Ala	Tyr	Val	Lys	Val	Asp	Ser	Cys	Pro	Glu	Glu	Pro	
			340					345					350			
Gln	Leu	Arg	Met	Lys	Asn	Asn	Glu	Glu	Ala	Glu	Asp	Tyr	Asp	Asp	Asp	
		355					360					365				
Leu	Thr	Asp	Ser	Glu	Met	Asp	Val	Val	Arg	Phe	Asp	Asp	Asp	Asn	Ser	
	370					375					380					
Pro	Ser	Phe	Ile	Gln	Ile	Arg	Ser	Val	Ala	Lys	Lys	His	Pro	Lys	Thr	
385					390					395					400	
Trp	Val	His	Tyr	Ile	Ala	Ala	Glu	Glu	Glu	Asp	Trp	Asp	Tyr	Ala	Pro	
				405					410					415		
Leu	Val	Leu	Ala	Pro	Asp	Asp	Arg	Ser	Tyr	Lys	Ser	Gln	Tyr	Leu	Asn	
			420					425					430			
Asn	Gly	Pro	Gln	Arg	Ile	Gly	Arg	Lys	Tyr	Lys	Lys	Val	Arg	Phe	Met	
		435					440					445				
Ala	Tyr	Thr	Asp	Glu	Thr	Phe	Lys	Thr	Arg	Glu	Ala	Ile	Gln	His	Glu	
	450					455					460					
Ser	Gly	Ile	Leu	Gly	Pro	Leu	Leu	Tyr	Gly	Glu	Val	Gly	Asp	Thr	Leu	
465					470					475					480	
Leu	Ile	Ile	Phe	Lys	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Asn	Ile	Tyr	Pro	
				485					490					495		
His	Gly	Ile	Thr	Asp	Val	Arg	Pro	Leu	Tyr	Ser	Arg	Arg	Leu	Pro	Lys	
			500					505					510			
Gly	Val	Lys	His	Leu	Lys	Asp	Phe	Pro	Ile	Leu	Pro	Gly	Glu	Ile	Phe	
		515					520					525				
Lys	Tyr	Lys	Trp	Thr	Val	Thr	Val	Glu	Asp	Gly	Pro	Thr	Lys	Ser	Asp	
	530					535					540					
Pro	Arg	Cys	Leu	Thr	Arg	Tyr	Tyr	Ser	Ser	Phe	Val	Asn	Met	Glu	Arg	
545					550					555					560	
Asp	Leu	Ala	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Ile	Cys	Tyr	Lys	Glu	
				565					570					575		
Ser	Val	Asp	Gln	Arg	Gly	Asn	Gln	Ile	Met	Ser	Asp	Lys	Arg	Asn	Val	
			580					585					590			
Ile	Leu	Phe	Ser	Val	Phe	Asp	Glu	Asn	Arg	Ser	Trp	Tyr	Leu	Thr	Glu	
	595						600					605				
Asn	Ile	Gln	Arg	Phe	Leu	Pro	Asn	Pro	Ala	Gly	Val	Gln	Leu	Glu	Asp	
	610					615					620					
Pro	Glu	Phe	Gln	Ala	Ser	Asn	Ile	Met	His	Ser	Ile	Asn	Gly	Tyr	Val	
625					630					635					640	
Phe	Asp	Ser	Leu	Gln	Leu	Ser	Val	Cys	Leu	His	Glu	Val	Ala	Tyr	Trp	
				645					650					655		
Tyr	Ile	Leu	Ser	Ile	Gly	Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe	
		660						665					670			
Ser	Gly	Tyr	Thr	Phe	Lys	His	Lys	Met	Val	Tyr	Glu	Asp	Thr	Leu	Thr	
		675					680					685				

Leu	Phe	Pro	Phe	Ser	Gly	Glu	Thr	Val	Phe	Met	Ser	Met	Glu	Asn	Pro	690	695	700
Gly	Leu	Trp	Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly	705	710	715
Met	Thr	Ala	Leu	Leu	Lys	Val	Ser	Ser	Cys	Asp	Lys	Asn	Thr	Gly	Asp	725	730	735
Tyr	Tyr	Glu	Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	Tyr	Leu	Leu	Ser	Lys	740	745	750
Asn	Asn	Ala	Ile	Glu	Pro	Arg	Ser	Phe	Ser	Gln	Asn	Ser	Arg	His	Pro	755	760	765
Ser	Thr	Arg	Gln	Lys	Gln	Phe	Asn	Ala	Thr	Pro	Pro	Val	Leu	Lys	Arg	770	775	780
His	Gln	Arg	Glu	Ile	Thr	Arg	Thr	Thr	Leu	Gln	Ser	Asp	Gln	Glu	Glu	785	790	795
Ile	Asp	Tyr	Asp	Asp	Thr	Ile	Ser	Val	Glu	Met	Lys	Lys	Glu	Asp	Phe	805	810	815
Asp	Ile	Tyr	Asp	Glu	Asp	Glu	Asn	Gln	Ser	Pro	Arg	Ser	Phe	Gln	Lys	820	825	830
Lys	Thr	Arg	His	Tyr	Phe	Ile	Ala	Ala	Val	Glu	Arg	Leu	Trp	Asp	Tyr	835	840	845
Gly	Met	Ser	Ser	Ser	Pro	His	Val	Leu	Arg	Asn	Arg	Ala	Gln	Ser	Gly	850	855	860
Ser	Val	Pro	Gln	Phe	Lys	Lys	Val	Val	Phe	Gln	Glu	Phe	Thr	Asp	Gly	865	870	875
Ser	Phe	Thr	Gln	Pro	Leu	Tyr	Arg	Gly	Glu	Leu	Asn	Glu	His	Leu	Gly	885	890	895
Leu	Leu	Gly	Pro	Tyr	Ile	Arg	Ala	Glu	Val	Glu	Asp	Asn	Ile	Met	Val	900	905	910
Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Ser	Phe	Tyr	Ser	Ser	Leu	915	920	925
Ile	Ser	Tyr	Glu	Glu	Asp	Gln	Arg	Gln	Gly	Ala	Glu	Pro	Arg	Lys	Asn	930	935	940
Phe	Val	Lys	Pro	Asn	Glu	Thr	Lys	Thr	Tyr	Phe	Trp	Lys	Val	Gln	His	945	950	955
His	Met	Ala	Pro	Thr	Lys	Asp	Glu	Phe	Asp	Cys	Lys	Ala	Trp	Ala	Tyr	965	970	975
Phe	Ser	Asp	Val	Asp	Leu	Glu	Lys	Asp	Val	His	Ser	Gly	Leu	Ile	Gly	980	985	990
Pro	Leu	Leu	Val	Cys	His	Thr	Asn	Thr	Leu	Asn	Pro	Ala	His	Gly	Arg	995	1000	1005
Gln	Val	Thr	Val	Gln	Glu	Phe	Ala	Leu	Phe	Phe	Thr	Ile	Phe	Asp	Glu	1010	1015	1020
Thr	Lys	Ser	Trp	Tyr	Phe	Thr	Glu	Asn	Met	Glu	Arg	Asn	Cys	Arg	Ala	1025	1030	1035
Pro	Cys	Asn	Ile	Gln	Met	Glu	Asp	Pro	Thr	Phe	Lys	Glu	Asn	Tyr	Arg	1045	1050	1055
Phe	His	Ala	Ile	Asn	Gly	Tyr	Ile	Met	Asp	Thr	Leu	Pro	Gly	Leu	Val	1060	1065	1070
Met	Ala	Gln	Asp	Gln	Arg	Ile	Arg	Trp	Tyr	Leu	Leu	Ser	Met	Gly	Ser	1075	1080	1085
Asn	Glu	Asn	Ile	His	Ser	Ile	His	Phe	Ser	Gly	His	Val	Phe	Thr	Val	1090	1095	1100
Arg	Lys	Lys	Glu	Glu	Tyr	Lys	Met	Ala	Leu	Tyr	Asn	Leu	Tyr	Pro	Gly	1105	1110	1115
Val	Phe	Glu	Thr	Val	Glu	Met	Leu	Pro	Ser	Lys	Ala	Gly	Ile	Trp	Arg	1125	1130	1135

<400> 3

```
tggccactcc ctctctgcgc gctcgtcgc tcaactgaggc cgggcgacca aaggtcgccc 60
gacgcccggg ctttgcccgg gcggcctcag tgagcgagcg agcgcgcaga gagggagtgg 120
ccaactccat cactaggggt tcctcagatc tctttctaag taaacagtac atgaaccttt 180
accccggttc tcggcaacgg cctgggtctgt gccaaagtgtt tgctgacgca acccccactg 240
gctggggcctt ggccataggc catcagcgca tgcggatctc agtgtgggtt tgcaagagga 300
agcaaaaagc ctctccaccc aggcctggaa tggttccacc caatgtcgag cagtgtgggt 360
ttgcaagagg aagcaaaaag cctctccacc caggcctgga ctcgacctcg agagtacttc 420
tagaaatacg agcc atg caa gta gag ctc tac acc tgc tgc ttt ctg tgc 470
                Met Gln Val Glu Leu Tyr Thr Cys Cys Phe Leu Cys
                  1             5             10
```

```
ctt ttg ccc ttc agc ctt agt gcc acc aga aaa tac tac ctc ggt gca 518
Leu Leu Pro Phe Ser Leu Ser Ala Thr Arg Lys Tyr Tyr Leu Gly Ala
                15             20             25
```

```
gtg gaa ctg tcc tgg gac tat atg caa agt gac ctg ctc agt gcg ctg 566
Val Glu Leu Ser Trp Asp Tyr Met Gln Ser Asp Leu Leu Ser Ala Leu
                30             35             40
```

```
cac gcg gat aca agc ttt tct tcc agg gtg cca gga tct ttg cca ctc 614
His Ala Asp Thr Ser Phe Ser Ser Arg Val Pro Gly Ser Leu Pro Leu
                45             50             55             60
```

```
acc acg tca gtc acg tac aga aag act gtg ttt gta gag ttt aca gat 662
Thr Thr Ser Val Thr Tyr Arg Lys Thr Val Phe Val Glu Phe Thr Asp
                65             70             75
```

```
gac ctt ttc aac att gcc aag ccc agg cca ccg tgg atg ggc ctg ctg 710
Asp Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu
                80             85             90
```

```
ggc cct acc atc cag gct gag gtt tat gac aca gtg gtc att gtc ctt 758
Gly Pro Thr Ile Gln Ala Glu Val Tyr Asp Thr Val Val Ile Val Leu
                95             100             105
```

```
aag aac atg gct tct cat cct gtc agc ctt cac gct gtt ggt gta tcc 806
Lys Asn Met Ala Ser His Pro Val Ser Leu His Ala Val Gly Val Ser
                110             115             120
```

```
tat tgg aaa gct tct gaa ggt gct gag tat gag gat cag acc agc caa 854
Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr Glu Asp Gln Thr Ser Gln
                125             130             135             140
```

```
aag gag aag gaa gat gat aat gtc att cct ggt gaa agc cat acc tat 902
Lys Glu Lys Glu Asp Asp Asn Val Ile Pro Gly Glu Ser His Thr Tyr
                145             150             155
```

```
gtc tgg cag gtc ctg aaa gag aat ggc cca atg gcc tct gat cca cca 950
Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Pro
                160             165             170
```

```
tgt ctc acc tac tca tat ttt tca cac gtg gac ctg gtg aaa gac ctg 998
Cys Leu Thr Tyr Ser Tyr Phe Ser His Val Asp Leu Val Lys Asp Leu
                175             180             185
```

aat tca ggc ctc att gga gcc ctg ctg gtt tgc aaa gaa ggg agt ctg	1046
Asn Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Lys Glu Gly Ser Leu	
190 195 200	
gcc aaa gaa agg aca cag acc ttg cag gaa ttt gtc cta ctt ttt gct	1094
Ala Lys Glu Arg Thr Gln Thr Leu Gln Glu Phe Val Leu Leu Phe Ala	
205 210 215 220	
gta ttt gat gaa ggg aaa agt tgg cac tca gaa aca aat gcg tct ttg	1142
Val Phe Asp Glu Gly Lys Ser Trp His Ser Glu Thr Asn Ala Ser Leu	
225 230 235	
aca cag gct gag gcc cag cat gag ctg cac acc atc aat ggc tat gta	1190
Thr Gln Ala Glu Ala Gln His Glu Leu His Thr Ile Asn Gly Tyr Val	
240 245 250	
aac agg tct ctg cca ggt ctt act gtg tgt cac aag aga tca gtc tat	1238
Asn Arg Ser Leu Pro Gly Leu Thr Val Cys His Lys Arg Ser Val Tyr	
255 260 265	
tgg cat gtg att gga atg ggc acc acc ccc gaa gtg cac tca att ttt	1286
Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe	
270 275 280	
ctc gaa ggt cac aca ttt ctt gtg agg aac cac cgc cag gcc tcc ttg	1334
Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu	
285 290 295 300	
gag atc tca cca att act ttc ctt act gct cag aca ttc ctg atg gac	1382
Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Phe Leu Met Asp	
305 310 315	
ctt ggc cag ttt cta ctg ttt tgt cat atc cct tcc cat caa cat gat	1430
Leu Gly Gln Phe Leu Leu Phe Cys His Ile Pro Ser His Gln His Asp	
320 325 330	
ggt atg gaa gct tat gtc aaa gta gat agc tgc cca gag gaa ccc cag	1478
Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln	
335 340 345	
ctg cgc atg aaa aat aat gaa gat aaa gat tat gat gat ggt ctt tat	1526
Leu Arg Met Lys Asn Asn Glu Asp Lys Asp Tyr Asp Asp Gly Leu Tyr	
350 355 360	
gat tct gac atg gac gta gtt agc ttt gat gac gac agc tct tct ccc	1574
Asp Ser Asp Met Asp Val Val Ser Phe Asp Asp Asp Ser Ser Ser Pro	
365 370 375 380	
ttt atc caa atc cgc tca gtt gcc aag aag cat cct aaa act tgg gtc	1622
Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val	
385 390 395	
cac tat att gct gct gag gag gag gac tgg gac tat gct ccc tca ggc	1670
His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Ser Gly	
400 405 410	

ccc acc ccc aat gat aga agt cat aaa aat ctg tat ttg aac aat ggt	1718
Pro Thr Pro Asn Asp Arg Ser His Lys Asn Leu Tyr Leu Asn Asn Gly	
415 420 425	
cct cag cgg att ggt aag aag tac aaa aaa gtc cga ttt gtg gca tac	1766
Pro Gln Arg Ile Gly Lys Lys Tyr Lys Lys Val Arg Phe Val Ala Tyr	
430 435 440	
aca gat gag aca ttt aag act cgt gaa gct att cag tat gaa tca gga	1814
Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln Tyr Glu Ser Gly	
445 450 455 460	
atc ctg gga cct tta ctt tat gga gaa gtt gga gac aca ctg ctg att	1862
Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile	
465 470 475	
ata ttt aag aat caa gcc agc cgg cca tat aac atc tac cct cat ggg	1910
Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly	
480 485 490	
atc aat tat gtc act cct ctg cac aca ggg aga ttg cca aaa ggt gtg	1958
Ile Asn Tyr Val Thr Pro Leu His Thr Gly Arg Leu Pro Lys Gly Val	
495 500 505	
aaa cat ttg aaa gat atg cca att ctg ccg gga gag ata ttc aag tat	2006
Lys His Leu Lys Asp Met Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr	
510 515 520	
aaa tgg aca gtg acc gta gaa gat gga cca act aaa tca gat cct cgg	2054
Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg	
525 530 535 540	
tgc ctg acc cga tat tac tca agc ttc att aat ctg gag aga gat cta	2102
Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Ile Asn Leu Glu Arg Asp Leu	
545 550 555	
gct tca gga ctc att ggc cct ctt ctc atc tgc tac aaa gaa tct gta	2150
Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val	
560 565 570	
gat caa aga gga aac cag atg atg tca gac aag aga aat gtc atc ctg	2198
Asp Gln Arg Gly Asn Gln Met Met Ser Asp Lys Arg Asn Val Ile Leu	
575 580 585	
ttt tct gta ttt gat gag aat cga agc tgg tac ctc aca gag aat atg	2246
Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Met	
590 595 600	
cag cgc ttc ctc ccc aat gca gat gta gtg cag ccc cat gac cca gag	2294
Gln Arg Phe Leu Pro Asn Ala Asp Val Val Gln Pro His Asp Pro Glu	
605 610 615 620	
ttc caa ctc tct aac atc atg cac agc atc aat ggc tat gtt ttt gac	2342
Phe Gln Leu Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp	
625 630 635	

aac ttg cag ctg tca gtt tgt ttg cat gag gtg gcg tac tgg tac att	2390
Asn Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile	
640 645 650	
cta agt gtt gga gca caa act gac ttc ctg tct gtc ttc ttc tct gga	2438
Leu Ser Val Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly	
655 660 665	
tat acc ttc aaa cac aaa atg gtc tat gaa gac aca ctt acc ctc ttc	2486
Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe	
670 675 680	
cca ttc tca gga gaa act gtc ttc atg tca atg gaa aac cca ggt ctg	2534
Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu	
685 690 695 700	
tgg gtt ctg ggg tgc cac aac tca gac ttt cgg aac aga ggc atg aca	2582
Trp Val Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr	
705 710 715	
gcc tta ctg aag gtt tct agt tgt aac agg aac att gat gat tat tat	2630
Ala Leu Leu Lys Val Ser Ser Cys Asn Arg Asn Ile Asp Asp Tyr Tyr	
720 725 730	
gag gac aca tac gaa gat att cca act ccc ctg cta aat gaa aac aat	2678
Glu Asp Thr Tyr Glu Asp Ile Pro Thr Pro Leu Leu Asn Glu Asn Asn	
735 740 745	
gta att aaa cct aga agc ttc tcc cag aat tca agg cac cct agc act	2726
Val Ile Lys Pro Arg Ser Phe Ser Gln Asn Ser Arg His Pro Ser Thr	
750 755 760	
aag gaa aag caa ttg aaa atg aag aga gaa gat ttt gac atc tac ggc	2774
Lys Glu Lys Gln Leu Lys Met Lys Arg Glu Asp Phe Asp Ile Tyr Gly	
765 770 775 780	
gac tat gaa aat cag ggc ctc cgc agc ttt caa aag aaa aca cga cac	2822
Asp Tyr Glu Asn Gln Gly Leu Arg Ser Phe Gln Lys Lys Thr Arg His	
785 790 795	
tat ttc att gct gca gtg gag cgt ctc tgg gat tat ggg atg agt aga	2870
Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser Arg	
800 805 810	
tct ccc cat ata cta aga aac agg gct caa agt ggg gat gtc cag cag	2918
Ser Pro His Ile Leu Arg Asn Arg Ala Gln Ser Gly Asp Val Gln Gln	
815 820 825	
ttc aag aag gtg gtt ttc cag gaa ttt act gat gga tcc ttt act cag	2966
Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln	
830 835 840	
ccc tta tac cgt gga gaa ctg aat gaa cac ttg gga ctc ttg ggg cca	3014
Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro	
845 850 855 860	

tat ata aga gca gaa gtt gaa gac aat atc gtg gta act ttc aaa aac	3062
Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Val Val Thr Phe Lys Asn	
865 870 875	
cag gcc tct cgt ccc tac tcc ttc tat tct agt ctt att tct tat gac	3110
Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Asp	
880 885 890	
gaa gat gag gga caa gga gca gaa cct aga aga aag ttt gtc aac cct	3158
Glu Asp Glu Gly Gln Gly Ala Glu Pro Arg Arg Lys Phe Val Asn Pro	
895 900 905	
aat gaa acc aaa att tac ttt tgg aaa gtg cag cat cat atg gca ccc	3206
Asn Glu Thr Lys Ile Tyr Phe Trp Lys Val Gln His His Met Ala Pro	
910 915 920	
act aaa gat gag ttt gac tgc aaa gcc tgg gct tat ttt tct gat gtt	3254
Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val	
925 930 935 940	
gat ttg gag aaa gat gtg cac tca ggc ttg att gga ccc ctt ctg atc	3302
Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Ile	
945 950 955	
tgc cgc agt aac aca ctg aac cct gct cat ggg aga caa gtg aca gtg	3350
Cys Arg Ser Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val	
960 965 970	
cag gag ttt gcc ctg gtt ttc act ata ttc gat gag act aag agc tgg	3398
Gln Glu Phe Ala Leu Val Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp	
975 980 985	
tac ttc act gaa aac ctg gaa agg aac tgt aga gct ccc tgc aat gtc	3446
Tyr Phe Thr Glu Asn Leu Glu Arg Asn Cys Arg Ala Pro Cys Asn Val	
990 995 1000	
cag aag gag gac cct act cta aaa gaa aac ttc cgc ttc cat gca atc	3494
Gln Lys Glu Asp Pro Thr Leu Lys Glu Asn Phe Arg Phe His Ala Ile	
1005 1010 1015 1020	
aac ggc tat gtg aag gat aca ctc cct ggc tta gta atg gct cag gat	3542
Asn Gly Tyr Val Lys Asp Thr Leu Pro Gly Leu Val Met Ala Gln Asp	
1025 1030 1035	
caa aag gtt cga tgg tat ctg ctc agc atg ggc agc aac gaa aac att	3590
Gln Lys Val Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn Ile	
1040 1045 1050	
cat tcc att cac ttc agt gga cat gtg ttc act gta cgg aaa aaa gag	3638
His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys Lys Glu	
1055 1060 1065	
gaa tat aaa atg gca gtc tac aac ctc tat cca ggt gtt ttt gag act	3686
Glu Tyr Lys Met Ala Val Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr	
1070 1075 1080	

gtg gaa atg cta cca tcc caa gtt gga atc tgg cgg ata gaa tgc ctt	3734
Val Glu Met Leu Pro Ser Gln Val Gly Ile Trp Arg Ile Glu Cys Leu	
1085 1090 1095 1100	
atc ggc gag cac ctg caa gcc ggg atg agc act ctg ttt ctg gtg tac	3782
Ile Gly Glu His Leu Gln Ala Gly Met Ser Thr Leu Phe Leu Val Tyr	
1105 1110 1115	
agc aag aag tgt cag act cca ctg ggg atg gct tcc gga cac att aga	3830
Ser Lys Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg	
1120 1125 1130	
gat ttt cag att aca gct tca gga caa tat gga cag tgg gcc cca aag	3878
Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys	
1135 1140 1145	
ctg gcc aga ctt cat tat tcc gga tca atc aat gcc tgg agc acc aag	3926
Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys	
1150 1155 1160	
gat ccc ttt tcc tgg atc aag gtg gat ctc ttg gca ccg atg att att	3974
Asp Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile Ile	
1165 1170 1175 1180	
cac ggc atc atg acc cag ggg gcc cgc cag aag ttc tcc agc ctc tac	4022
His Gly Ile Met Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr	
1185 1190 1195	
gtg tct cag ttt atc atc atg tac agt ctg gat ggc aac aag tgg cac	4070
Val Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Asn Lys Trp His	
1200 1205 1210	
agt tac cga ggg aat tcc acg ggg acc tta atg gtc ttc ttt ggc aac	4118
Ser Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn	
1215 1220 1225	
gtg gat tca tct ggg atc aaa cac aat att ttt aac cct ccg att att	4166
Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile Ile	
1230 1235 1240	
gct cag tac atc cgt ttg cac cca acc cat tac agc atc cgc agc act	4214
Ala Gln Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser Thr	
1245 1250 1255 1260	
ctt cgc atg gag ctc ttg ggc tgt gac ttc aac agt tgc agc atg ccg	4262
Leu Arg Met Glu Leu Leu Gly Cys Asp Phe Asn Ser Cys Ser Met Pro	
1265 1270 1275	
ctg ggg atg gag agt aaa gca ata tca gat gct cag atc act gcc tcg	4310
Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser	
1280 1285 1290	
tcc tac cta agc agt atg ctt gcc act tgg tct cct tcc caa gcc cgg	4358
Ser Tyr Leu Ser Ser Met Leu Ala Thr Trp Ser Pro Ser Gln Ala Arg	
1295 1300 1305	

ctg cac ctg cag ggc agg act aat gcc tgg aga cct cag gca aat aac	4406
Leu His Leu Gln Gly Arg Thr Asn Ala Trp Arg Pro Gln Ala Asn Asn	
1310 1315 1320	
cca aaa gag tgg ctg caa gtg gac ttc cgg aag acc atg aaa gtc aca	4454
Pro Lys Glu Trp Leu Gln Val Asp Phe Arg Lys Thr Met Lys Val Thr	
1325 1330 1335 1340	
gga ata acc acc cag ggg gtg aaa tct ctc ctc atc agc atg tat gtg	4502
Gly Ile Thr Thr Gln Gly Val Lys Ser Leu Leu Ile Ser Met Tyr Val	
1345 1350 1355	
aag gag ttc ctc atc tcc agt agt caa gat ggc cat aac tgg act ctg	4550
Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Asn Trp Thr Leu	
1360 1365 1370	
ttt ctt cag aat ggc aaa gtc aag gtc ttc cag gga aac cgg gac tcc	4598
Phe Leu Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn Arg Asp Ser	
1375 1380 1385	
tcc acg cct gtg cgg aac cgt ctc gaa ccc ccg ctg gtg gct cgc tac	4646
Ser Thr Pro Val Arg Asn Arg Leu Glu Pro Pro Leu Val Ala Arg Tyr	
1390 1395 1400	
gtg cgc ctg cac ccg cag agc tgg gcg cac cac atc gcc ctg agg ctg	4694
Val Arg Leu His Pro Gln Ser Trp Ala His His Ile Ala Leu Arg Leu	
1405 1410 1415 1420	
gag gtc ctg ggc tgc gac acc cag cag ccc gcc tga cccgcgcctc	4740
Glu Val Leu Gly Cys Asp Thr Gln Gln Pro Ala *	
1425 1430	
tgcggccctg tctccctgc ctccctgccc tgtccccgcg gcttcccatc aagcttatcg	4800
ataccgtcga gcgagttctt ctgaggggat cggcaataaa aagacagaat aaaacgcacg	4860
ggtgttggt cgtttgttcg gatccagatc taggaacccc tagtgatgga gttggccact	4920
ccctctctgc gcgctcgtc gctcactgag gccgcccggg caaagcccgg gcgtcgggcg	4980
acctttggtc gcccggcctc agtgagcgag cgagcgcgca gagagggagt ggccaacccc	5040
cccccccccc cccctgcagc ccagctgcat taatgaatcg gccaacgcgc ggggagaggc	5100
ggtttgcgta ttgggcgctc ttccgcttcc tcgctcactg actcgtcgcg ctcggtcgtt	5160
cggctgcggc gagcggatc agctcactca aaggcggtaa tacggttatc cacagaatca	5220
ggggataacg caggaaagaa catgtgagca aaaggccagc aaaaggccag gaaccgtaaa	5280
aaggccgcgt tgctggcggt tttccatagg ctccgcccc ctgacgagca tcacaaaaat	5340
cgacgctcaa gtcagagggt gcgaaacccg acaggactat aaagatacca ggcgtttccc	5400
cctggaagct cctcgtgcg ctctcctgtt ccgacctgc cgcttaccgg atacctgtcc	5460
gcctttctcc cttcggaag cgtggcgctt tctcaatgct cacgctgtag gtatctcagt	5520
tcggtgtagg tcgttcgctc caagctgggc tgtgtgcacg aacccccgt tcagcccgac	5580
cgctgcgcct tatccggtaa ctatcgtctt gagtccaacc cggtaaagaca cgacttatcg	5640
ccactggcag cagccactgg taacaggatt agcagagcga ggtatgtagg cgggtgctaca	5700
gagttcttga agtggtggcc taactacggc tacactagaa ggacagtatt tggatatctgc	5760
gctctgctga agccagttac cttcggaata agagttggtg gctcttgatc cggcaaaaca	5820
accacgcgtg gtacgcgttg tttttttgtt tgcaagcagc agattacgcg cagaaaaaaa	5880
ggatctcaag aagatccttt gatcttttct acgggggtctg acgctcagtg gaacgaaaac	5940
tcacgttaag ggatttttgt catgagatta tcaaaaagga tcttcacctg gatcctttta	6000
aattaaaaat gaagttttta atcaatctaa agtatatatg agtaaaacttg gtctgacagt	6060
taccaatgct taatcagtga ggcacctatc tcagcgatct gtctatttcg ttcattcata	6120
gttgccctgac tccccgctgt gtagataact acgatacggg agggcttacc atctggcccc	6180

```

agtgtgcaa tgataccgag agaccacgc tcaccggctc cagattttatc agcaataaac 6240
cagccagccg gaagggccga gcgcagaagt ggtcctgcaa ctttatccgc ctccatccag 6300
tctattaatt gttgccggga agctagagta agtagttcgc cagttaatag tttgcgcaac 6360
gttgttgcca ttgctacagg catcgtggtg tcacgctcgt cgtttggtat ggcttcattc 6420
agctccggtt cccaacgata aaggcgagtt acatgatccc ccatgttggtg caaaaaagcg 6480
gttagctcct tcggctcctcc gatcgttggtc agaagtaagt tggccgcagt gttatcactc 6540
atggttatgg cagcactgca taattctctt actgtcatgc catccgtaag atgcttttct 6600
gtgactggtg agtactcaac caagtcattc tgagaatagt gtatgcggcg accgagttgc 6660
tcttgcccgg cgtcaatacg ggataatacc gcgccacata gcagaacttt aaaagtgtc 6720
atcattggaa aacgttcttc ggggcgaaaa ctctcaagga tcttaccgct gttgagatcc 6780
agttcgatgt aaccactcgc tgcacccaac tgatcttcag catcttttac tttcaccagc 6840
gtttctgggt gagcaaaaaac aggaaggcaa aatgccgcaa aaaagggaaat aagggcgaca 6900
cggaatatgt gaatactcat actcttcctt tttcaatatt attgaagcat ttatcagggt 6960
tattgtctca tgagcgggata catatttgaa tgtattttaga aaaataaaca aataggggtt 7020
ccgcgcacat ttccccgaaa agtgccacct gacgtctaag aaaccattat tatcatgaca 7080
ttaacctata aaaataggcg tatcacgagg ccctttcgtc tcgcgcgttt cggatgatgac 7140
ggtgaaaacc tctgacacat gcagctcccg gagacggtca cagcttgtct gtaagcggat 7200
gccgggagca gacaagcccgc tcagggcgcg tcagcgggtg ttggcgggtg tcggggctg 7260
cttaactatg cggcatcaga gcagattgta ctgagagtgc accatatgcg gtgtgaaata 7320
ccgcacagat gcgtaaggag aaaataccgc atcaggaaat tgtaaacgtt aatattttgt 7380
taaaattcgc gttaaatttt tgtaaataca gctcattttt taaccaatag gccgaaatcg 7440
gcaaaatccc ttataaatca aaagaataga ccgagatagg gttgagtgtt gttccagttt 7500
ggaacaagag tccactatta aagaacgtgg actccaacgt caaagggcga aaaaccgtct 7560
atcagggcga tggcccacta cgtgaaccat caccctaatac aagttttttg gggtcgaggt 7620
gccgtaaaag actaaatcgg aaccctaaag ggagcccccg atttagagct tgacggggaa 7680
agccggcgaa cgtggcgaga aaggaaggga agaaagcgaa aggagcgggc gctagggcgc 7740
tggcaagtgt agcgtcacg ctgcgcgtaa ccaccacacc cgccgcgctt aatgcgccgc 7800
tacagggcgc gtcgcgccat tcgccattca ggctacgcaa ctgttgggaa gggcgatcgc 7860
tgccggcctc ttcgctatta cgccagctgg ctgcaggggg gggggggggg ggg 7914

```

<210> 4

<211> 1431

<212> PRT

<213> canine B-domain deleted factor VIII

<400> 4

```

Met Gln Val Glu Leu Tyr Thr Cys Cys Phe Leu Cys Leu Leu Pro Phe
 1             5             10             15
Ser Leu Ser Ala Thr Arg Lys Tyr Tyr Leu Gly Ala Val Glu Leu Ser
 20             25             30
Trp Asp Tyr Met Gln Ser Asp Leu Leu Ser Ala Leu His Ala Asp Thr
 35             40             45
Ser Phe Ser Ser Arg Val Pro Gly Ser Leu Pro Leu Thr Thr Ser Val
 50             55             60
Thr Tyr Arg Lys Thr Val Phe Val Glu Phe Thr Asp Asp Leu Phe Asn
 65             70             75             80
Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile
 85             90             95
Gln Ala Glu Val Tyr Asp Thr Val Val Ile Val Leu Lys Asn Met Ala
 100            105            110
Ser His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala
 115            120            125
Ser Glu Gly Ala Glu Tyr Glu Asp Gln Thr Ser Gln Lys Glu Lys Glu
 130            135            140
Asp Asp Asn Val Ile Pro Gly Glu Ser His Thr Tyr Val Trp Gln Val
 145            150            155            160

```

Leu	Lys	Glu	Asn	Gly	Pro	Met	Ala	Ser	Asp	Pro	Pro	Cys	Leu	Thr	Tyr	
				165					170					175		
Ser	Tyr	Phe	Ser	His	Val	Asp	Leu	Val	Lys	Asp	Leu	Asn	Ser	Gly	Leu	
			180					185				190				
Ile	Gly	Ala	Leu	Leu	Val	Cys	Lys	Glu	Gly	Ser	Leu	Ala	Lys	Glu	Arg	
		195					200					205				
Thr	Gln	Thr	Leu	Gln	Glu	Phe	Val	Leu	Leu	Phe	Ala	Val	Phe	Asp	Glu	
	210					215					220					
Gly	Lys	Ser	Trp	His	Ser	Glu	Thr	Asn	Ala	Ser	Leu	Thr	Gln	Ala	Glu	
225					230					235					240	
Ala	Gln	His	Glu	Leu	His	Thr	Ile	Asn	Gly	Tyr	Val	Asn	Arg	Ser	Leu	
			245						250					255		
Pro	Gly	Leu	Thr	Val	Cys	His	Lys	Arg	Ser	Val	Tyr	Trp	His	Val	Ile	
		260						265					270			
Gly	Met	Gly	Thr	Thr	Pro	Glu	Val	His	Ser	Ile	Phe	Leu	Glu	Gly	His	
		275					280					285				
Thr	Phe	Leu	Val	Arg	Asn	His	Arg	Gln	Ala	Ser	Leu	Glu	Ile	Ser	Pro	
	290					295					300					
Ile	Thr	Phe	Leu	Thr	Ala	Gln	Thr	Phe	Leu	Met	Asp	Leu	Gly	Gln	Phe	
305					310					315					320	
Leu	Leu	Phe	Cys	His	Ile	Pro	Ser	His	Gln	His	Asp	Gly	Met	Glu	Ala	
			325						330					335		
Tyr	Val	Lys	Val	Asp	Ser	Cys	Pro	Glu	Glu	Pro	Gln	Leu	Arg	Met	Lys	
		340						345					350			
Asn	Asn	Glu	Asp	Lys	Asp	Tyr	Asp	Asp	Gly	Leu	Tyr	Asp	Ser	Asp	Met	
		355					360					365				
Asp	Val	Val	Ser	Phe	Asp	Asp	Asp	Ser	Ser	Ser	Pro	Phe	Ile	Gln	Ile	
	370					375					380					
Arg	Ser	Val	Ala	Lys	Lys	His	Pro	Lys	Thr	Trp	Val	His	Tyr	Ile	Ala	
385					390					395					400	
Ala	Glu	Glu	Glu	Asp	Trp	Asp	Tyr	Ala	Pro	Ser	Gly	Pro	Thr	Pro	Asn	
			405						410					415		
Asp	Arg	Ser	His	Lys	Asn	Leu	Tyr	Leu	Asn	Asn	Gly	Pro	Gln	Arg	Ile	
			420					425					430			
Gly	Lys	Lys	Tyr	Lys	Lys	Val	Arg	Phe	Val	Ala	Tyr	Thr	Asp	Glu	Thr	
		435					440					445				
Phe	Lys	Thr	Arg	Glu	Ala	Ile	Gln	Tyr	Glu	Ser	Gly	Ile	Leu	Gly	Pro	
	450					455					460					
Leu	Leu	Tyr	Gly	Glu	Val	Gly	Asp	Thr	Leu	Leu	Ile	Ile	Phe	Lys	Asn	
465					470					475					480	
Gln	Ala	Ser	Arg	Pro	Tyr	Asn	Ile	Tyr	Pro	His	Gly	Ile	Asn	Tyr	Val	
			485						490					495		
Thr	Pro	Leu	His	Thr	Gly	Arg	Leu	Pro	Lys	Gly	Val	Lys	His	Leu	Lys	
			500					505					510			
Asp	Met	Pro	Ile	Leu	Pro	Gly	Glu	Ile	Phe	Lys	Tyr	Lys	Trp	Thr	Val	
	515						520					525				
Thr	Val	Glu	Asp	Gly	Pro	Thr	Lys	Ser	Asp	Pro	Arg	Cys	Leu	Thr	Arg	
	530					535					540					
Tyr	Tyr	Ser	Ser	Phe	Ile	Asn	Leu	Glu	Arg	Asp	Leu	Ala	Ser	Gly	Leu	
545					550					555					560	
Ile	Gly	Pro	Leu	Leu	Ile	Cys	Tyr	Lys	Glu	Ser	Val	Asp	Gln	Arg	Gly	
			565						570					575		
Asn	Gln	Met	Met	Ser	Asp	Lys	Arg	Asn	Val	Ile	Leu	Phe	Ser	Val	Phe	
			580					585				590				
Asp	Glu	Asn	Arg	Ser	Trp	Tyr	Leu	Thr	Glu	Asn	Met	Gln	Arg	Phe	Leu	
		595					600					605				

Pro	Asn	Ala	Asp	Val	Val	Gln	Pro	His	Asp	Pro	Glu	Phe	Gln	Leu	Ser	610	615	620
Asn	Ile	Met	His	Ser	Ile	Asn	Gly	Tyr	Val	Phe	Asp	Asn	Leu	Gln	Leu	625	630	635
Ser	Val	Cys	Leu	His	Glu	Val	Ala	Tyr	Trp	Tyr	Ile	Leu	Ser	Val	Gly	645	650	655
Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe	Ser	Gly	Tyr	Thr	Phe	Lys	660	665	670
His	Lys	Met	Val	Tyr	Glu	Asp	Thr	Leu	Thr	Leu	Phe	Pro	Phe	Ser	Gly	675	680	685
Glu	Thr	Val	Phe	Met	Ser	Met	Glu	Asn	Pro	Gly	Leu	Trp	Val	Leu	Gly	690	695	700
Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly	Met	Thr	Ala	Leu	Leu	Lys	705	710	715
Val	Ser	Ser	Cys	Asn	Arg	Asn	Ile	Asp	Asp	Tyr	Tyr	Glu	Asp	Thr	Tyr	725	730	735
Glu	Asp	Ile	Pro	Thr	Pro	Leu	Leu	Asn	Glu	Asn	Asn	Val	Ile	Lys	Pro	740	745	750
Arg	Ser	Phe	Ser	Gln	Asn	Ser	Arg	His	Pro	Ser	Thr	Lys	Glu	Lys	Gln	755	760	765
Leu	Lys	Met	Lys	Arg	Glu	Asp	Phe	Asp	Ile	Tyr	Gly	Asp	Tyr	Glu	Asn	770	775	780
Gln	Gly	Leu	Arg	Ser	Phe	Gln	Lys	Lys	Thr	Arg	His	Tyr	Phe	Ile	Ala	785	790	795
Ala	Val	Glu	Arg	Leu	Trp	Asp	Tyr	Gly	Met	Ser	Arg	Ser	Pro	His	Ile	805	810	815
Leu	Arg	Asn	Arg	Ala	Gln	Ser	Gly	Asp	Val	Gln	Gln	Phe	Lys	Lys	Val	820	825	830
Val	Phe	Gln	Glu	Phe	Thr	Asp	Gly	Ser	Phe	Thr	Gln	Pro	Leu	Tyr	Arg	835	840	845
Gly	Glu	Leu	Asn	Glu	His	Leu	Gly	Leu	Leu	Gly	Pro	Tyr	Ile	Arg	Ala	850	855	860
Glu	Val	Glu	Asp	Asn	Ile	Val	Val	Thr	Phe	Lys	Asn	Gln	Ala	Ser	Arg	865	870	875
Pro	Tyr	Ser	Phe	Tyr	Ser	Ser	Leu	Ile	Ser	Tyr	Asp	Glu	Asp	Glu	Gly	885	890	895
Gln	Gly	Ala	Glu	Pro	Arg	Arg	Lys	Phe	Val	Asn	Pro	Asn	Glu	Thr	Lys	900	905	910
Ile	Tyr	Phe	Trp	Lys	Val	Gln	His	His	Met	Ala	Pro	Thr	Lys	Asp	Glu	915	920	925
Phe	Asp	Cys	Lys	Ala	Trp	Ala	Tyr	Phe	Ser	Asp	Val	Asp	Leu	Glu	Lys	930	935	940
Asp	Val	His	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Ile	Cys	Arg	Ser	Asn	945	950	955
Thr	Leu	Asn	Pro	Ala	His	Gly	Arg	Gln	Val	Thr	Val	Gln	Glu	Phe	Ala	965	970	975
Leu	Val	Phe	Thr	Ile	Phe	Asp	Glu	Thr	Lys	Ser	Trp	Tyr	Phe	Thr	Glu	980	985	990
Asn	Leu	Glu	Arg	Asn	Cys	Arg	Ala	Pro	Cys	Asn	Val	Gln	Lys	Glu	Asp	995	1000	1005
Pro	Thr	Leu	Lys	Glu	Asn	Phe	Arg	Phe	His	Ala	Ile	Asn	Gly	Tyr	Val	1010	1015	1020
Lys	Asp	Thr	Leu	Pro	Gly	Leu	Val	Met	Ala	Gln	Asp	Gln	Lys	Val	Arg	1025	1030	1035
Trp	Tyr	Leu	Leu	Ser	Met	Gly	Ser	Asn	Glu	Asn	Ile	His	Ser	Ile	His	1045	1050	1055

Phe	Ser	Gly	His	Val	Phe	Thr	Val	Arg	Lys	Lys	Glu	Glu	Tyr	Lys	Met	1060	1065	1070
Ala	Val	Tyr	Asn	Leu	Tyr	Pro	Gly	Val	Phe	Glu	Thr	Val	Glu	Met	Leu	1075	1080	1085
Pro	Ser	Gln	Val	Gly	Ile	Trp	Arg	Ile	Glu	Cys	Leu	Ile	Gly	Glu	His	1090	1095	1100
Leu	Gln	Ala	Gly	Met	Ser	Thr	Leu	Phe	Leu	Val	Tyr	Ser	Lys	Lys	Cys	1105	1110	1115
Gln	Thr	Pro	Leu	Gly	Met	Ala	Ser	Gly	His	Ile	Arg	Asp	Phe	Gln	Ile	1125	1130	1135
Thr	Ala	Ser	Gly	Gln	Tyr	Gly	Gln	Trp	Ala	Pro	Lys	Leu	Ala	Arg	Leu	1140	1145	1150
His	Tyr	Ser	Gly	Ser	Ile	Asn	Ala	Trp	Ser	Thr	Lys	Asp	Pro	Phe	Ser	1155	1160	1165
Trp	Ile	Lys	Val	Asp	Leu	Leu	Ala	Pro	Met	Ile	Ile	His	Gly	Ile	Met	1170	1175	1180
Thr	Gln	Gly	Ala	Arg	Gln	Lys	Phe	Ser	Ser	Leu	Tyr	Val	Ser	Gln	Phe	1185	1190	1195
Ile	Ile	Met	Tyr	Ser	Leu	Asp	Gly	Asn	Lys	Trp	His	Ser	Tyr	Arg	Gly	1205	1210	1215
Asn	Ser	Thr	Gly	Thr	Leu	Met	Val	Phe	Phe	Gly	Asn	Val	Asp	Ser	Ser	1220	1225	1230
Gly	Ile	Lys	His	Asn	Ile	Phe	Asn	Pro	Pro	Ile	Ile	Ala	Gln	Tyr	Ile	1235	1240	1245
Arg	Leu	His	Pro	Thr	His	Tyr	Ser	Ile	Arg	Ser	Thr	Leu	Arg	Met	Glu	1250	1255	1260
Leu	Leu	Gly	Cys	Asp	Phe	Asn	Ser	Cys	Ser	Met	Pro	Leu	Gly	Met	Glu	1265	1270	1275
Ser	Lys	Ala	Ile	Ser	Asp	Ala	Gln	Ile	Thr	Ala	Ser	Ser	Tyr	Leu	Ser	1285	1290	1295
Ser	Met	Leu	Ala	Thr	Trp	Ser	Pro	Ser	Gln	Ala	Arg	Leu	His	Leu	Gln	1300	1305	1310
Gly	Arg	Thr	Asn	Ala	Trp	Arg	Pro	Gln	Ala	Asn	Asn	Pro	Lys	Glu	Trp	1315	1320	1325
Leu	Gln	Val	Asp	Phe	Arg	Lys	Thr	Met	Lys	Val	Thr	Gly	Ile	Thr	Thr	1330	1335	1340
Gln	Gly	Val	Lys	Ser	Leu	Leu	Ile	Ser	Met	Tyr	Val	Lys	Glu	Phe	Leu	1345	1350	1355
Ile	Ser	Ser	Ser	Gln	Asp	Gly	His	Asn	Trp	Thr	Leu	Phe	Leu	Gln	Asn	1365	1370	1375
Gly	Lys	Val	Lys	Val	Phe	Gln	Gly	Asn	Arg	Asp	Ser	Ser	Thr	Pro	Val	1380	1385	1390
Arg	Asn	Arg	Leu	Glu	Pro	Pro	Leu	Val	Ala	Arg	Tyr	Val	Arg	Leu	His	1395	1400	1405
Pro	Gln	Ser	Trp	Ala	His	His	Ile	Ala	Leu	Arg	Leu	Glu	Val	Leu	Gly	1410	1415	1420
Cys	Asp	Thr	Gln	Gln	Pro	Ala										1425		1430

<210> 5

<211> 12

<212> DNA

<213> Artificial Sequence

<220>